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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT	PAPER NUMBER
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DATE MAILED:

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OCT 19 2001
TECH CENTER 1600/2900

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Docketed 8/30/01 Attorney DAM/LAM/MTL
Case 1142-122
Due Date 9/29/01 w/EXT
Action SEQUENCE LISTING DUE
By [Signature] 8/30/01

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AUG 30 2001

FINNEGAN, HENDERSON,
FARABOW, GARRETT & BUNNER, L.L.P.



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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
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EXAMINER

ART UNIT	PAPER NUMBER
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29

DATE MAILED:

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OCT 19 2001
TECH CENTER 1600/2900

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

Serial No. 08/816,011

1. The reply filed 11 June 2001 (Paper No. 28) is not fully responsive to the communication mailed 11 May 2001 (Paper No. 27) for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report.

Since the above-mentioned reply appears to be *bona fide*, applicant is given a TIME PERIOD of ONE (1) MONTH or THIRTY (30) DAYS, from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME LIMIT MAY BE GRANTED UNDER 37 CFR 1.136(a).

2. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Michael Pak, whose telephone number is (703) 305-7038. The examiner can normally be reached on Monday through Friday from 8:30 AM to 2:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler, can be reached on (703) 308-6564.

Official papers filed by fax should be directed to (703) 308-4242. Faxed draft or informal communications with the examiner should be directed to (703) 308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Michael D. Pak
Michael Pak
Primary Patent Examiner
Art Unit 1646
16 August 2001

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114-OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

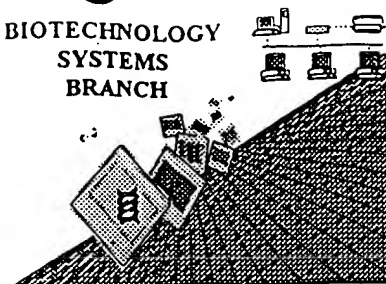
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17-00000
N. Park

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**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 08/816,011D
Source: OIPK
Date Processed by STIC: 6/25/2001

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OCT 19 2001
TECHCENTER 1600/2330

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTIONSERIAL NUMBER: 08/8/6,011D

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence
- 11 ✓ Use of <220> Sequence(s) 65 missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

Does Not Comply
Corrected Diskette Needed
P. 6

3 <110> APPLICANT: Pausch, Mark H
4 Price, Laura A
6 <120> TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
7 AND METHODS OF USING SAME
9 <130> FILE REFERENCE: 01142.0122 SEQUENCE LISTING
11 <140> CURRENT APPLICATION NUMBER: 08/816,011D
C--> 12 <141> CURRENT FILING DATE: 2001-06-11
14 <150> PRIOR APPLICATION NUMBER: 08/332,312
15 <151> PRIOR FILING DATE: 1994-10-31
17 <150> PRIOR APPLICATION NUMBER: PCT/US95/14364
18 <151> PRIOR FILING DATE: 1995-10-25
20 <160> NUMBER OF SEQ ID NOS: 67
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2441
26 <212> TYPE: DNA
27 <213> ORGANISM: Drosophila melanogaster
29 <400> SEQUENCE: 1
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31 ctttaaaaga aaaaaaaaaat aataagtcaa aactacaaac cacacagcga aaggcgaaag 120
32 caacgggtcc tgcgagtgtt tatttttttt ttcaacaatt tttgatcgta gtgcgacaat 180
33 ccgtcgagca tgcgcgcgaa tcgatggatc ctgctgctca tcttctacat atcctacctg 240
34 atgttcgggg cggaatcta ttaccatatt gagcacggcg aggagaagat atcgcgggcc 300
35 gaacagcgca aggcgcaaat tgcaatcaac gaatatctgc tggaggagct gggcgacaag 360
36 aatacgacca cacaggatga gattcttcaa cggatctcgg attactgtga caaaccgggt 420
37 acattgccgc cgacatatga tgatacggcc tacacgtgga ccttctacca tgccttcttc 480
38 ttgccttca ccgtttgctc cacgggtgga tatgggaata tatcgccaac cacttcgcc 540
39 ggacggatga tcatgatcgc gtattcgggtg attggcatcc ccgtcaatgg tatcctcttt 600
40 gccggcctcg gcgaatactt tggacgtacg tttgaagcga tctacagacg ctacaaaag 660
41 tacaagatgt ccacggatat gcactatgtc ccgcgcgagc tgggattgat caccacgggtg 720
42 gtgattgccc tgattccggg aatagctctc ttcttggtgc tgcctgcgt ggggtgtcac 780
43 ctacttcgag aactgggcct atcttccatc tcgctgtact acagctatgt gaccaccaca 840
44 acaattggat tcggtgacta tgtgccca tttggagcca accagcccaa ggagttcggc 900
45 ggctggttcg tgggtctatca gatctttgtg atcgtgtggt tcatcttctc gctgggatat 960
46 cttgtgatga tcatgacatt tatcactcgg ggcctccaga gcaagaagct ggcatacctg 1020
47 gagcagcagt tgctctccaa cctgaaggcc acacagaatc gcatctggtc tggcgccacc 1080
48 aaggatgtgg gctacctccg gcgaatgtc aacgagctgt acatcctcaa agtgaagcct 1140
49 gtgtacaccg atgtagatat cgctacaca ctgccacgtt ccaattcgtg tccggatctg 1200
50 agcatgtacc gcgtggagcc ggctcccat cccagccgga agagggcatt ctccgtgtgc 1260
51 gccgacatgg ttggcgccca aagggaggcg ggcattggtac acgccaattc cgatacggat 1320
52 ctaaccaaac tggatcgcca gaagacattc gagacggcgg aggcgtacca ccagaccacc 1380
53 gatttgctgg ccaagggtgt caacgcactg gccacgggtga agccaccgcc ggcggaacag 1440
54 gaagatgcgg ctctctatgg tggctatcat ggcttctccg actcccagat cctggccagc 1500
55 gaatggtcgt tctcgacggg caacgagttc acatcaccgc gacgtccaag agcacgtgcc 1560
56 tgctccgatt tcaatctgga ggcacctcgc tggcagagcg agaggccact gcgttcgagc 1620
57 cacaacgaat ggacatggag cggcgacaac cagcagatcc aggaggcatt caaccagcgc 1680
58 tacaagggac agcagcgtgc caacggagca gccaaactcga ccatggtcca tctggagccg 1740

RAW SEQUENCE LISTING

DATE: 06/25/2001

PATENT APPLICATION: US/08/816,011D

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

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59 gatgcttttg aggagcagct gagaaacaat caccgggtgc cggtcgctgc aagaagtctt 1800
60 ccatgccgga tggctgcga cgtctgtttc cttccagaa gaagcaccctc tcgcaggatc 1860
61 tggagcgcaa gttgtccgtg gtctcggtac ccgagggtgt catctcgag gaagccagat 1920
62 ccccgtgga ctactacatc aacacggtca cggcggcctc cagtcaatcc tatttgcgca 1980
63 acggacgcgg tccgccaccg cccttcgaat cgaatggcag cttggccagc ggcggcgcg 2040
64 ggctaacgaa catgggcttc cagatggagg atggagcaac cccgccatcg gcattggcg 2100
65 gtggagccta tcaacgcaag gcggtcgtg gcaagcgccg acgcgagagc atctacacc 2160
66 agaataaagc cccatccgct cgcgggggca gcatgtatcc gccgaccgcg dacgccttg 2220
67 cccagatgca gatgcgacgc ggcagcttg caaccagtgg ctctggatcg gcggccatgg 2280
68 cggcagtggc cgcgcgtcgt ggcagcctt tcccagctac agcatcgga tcatcgctga 2340
69 cctctgctcc gcgccgaagc agcatattct cggttacctc cgaaaaggat atgaatgtgc 2400
70 tggagcagac gaccattgcg gatctgattc gtgcgctcga g 2441

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73 <210> SEQ ID NO: 2

74 <211> LENGTH: 618

75 <212> TYPE: PRT

76 <213> ORGANISM: Drosophila melanogaster

78 <400> SEQUENCE: 2

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80 1 5 10 15
82 Leu Met Phe Gly Ala Ala Ile Tyr Tyr His Ile Glu His Gly Glu Glu
83 20 25 30
85 Lys Ile Ser Arg Ala Glu Gln Arg Lys Ala Gln Ile Ala Ile Asn Glu
86 35 40 45
88 Tyr Leu Leu Glu Glu Leu Gly Asp Lys Asn Thr Thr Thr Gln Asp Glu
89 50 55 60
91 Ile Leu Gln Arg Ile Ser Asp Tyr Cys Asp Lys Pro Val Thr Leu Pro
92 65 70 75 80
94 Pro Thr Tyr Asp Asp Thr Pro Tyr Thr Trp Thr Phe Tyr His Ala Phe
95 85 90 95
97 Phe Phe Ala Phe Thr Val Cys Ser Thr Val Gly Tyr Gly Asn Ile Ser
98 100 105 110
100 Pro Thr Thr Phe Ala Gly Arg Met Ile Met Ile Ala Tyr Ser Val Ile
101 115 120 125
103 Gly Ile Pro Val Asn Gly Ile Leu Phe Ala Gly Leu Gly Glu Tyr Phe
104 130 135 140
106 Gly Arg Thr Phe Glu Ala Ile Tyr Arg Arg Tyr Lys Lys Tyr Lys Met
107 145 150 155 160
109 Ser Thr Asp Met His Tyr Val Pro Pro Gln Leu Gly Leu Ile Thr Thr
110 165 170 175
112 Val Val Ile Ala Leu Ile Pro Gly Ile Ala Leu Phe Leu Val Leu Pro
113 180 185 190
115 Cys Val Gly Val His Leu Leu Arg Glu Leu Gly Leu Ser Ser Ile Ser
116 195 200 205
118 Leu Tyr Tyr Ser Tyr Val Thr Thr Thr Thr Ile Gly Phe Gly Asp Tyr
119 210 215 220
121 Val Pro Thr Phe Gly Ala Asn Gln Pro Lys Glu Phe Gly Gly Trp Phe
122 225 230 235 240
124 Val Val Tyr Gln Ile Phe Val Ile Val Trp Phe Ile Phe Ser Leu Gly
125 245 250 255

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

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127 Tyr Leu Val Met Ile Met Thr Phe Ile Thr Arg Gly Leu Gln Ser Lys
128           260           265           270
130 Lys Leu Ala Tyr Leu Glu Gln Gln Leu Ser Ser Asn Leu Lys Ala Thr
131           275           280           285
133 Gln Asn Arg Ile Trp Ser Gly Val Thr Lys Asp Val Gly Tyr Leu Arg
134           290           295           300
136 Arg Met Leu Asn Glu Leu Tyr Ile Leu Lys Val Lys Pro Val Tyr Thr
137 305           310           315           320
139 Asp Val Asp Ile Ala Tyr Thr Leu Pro Arg Ser Asn Ser Cys Pro Asp
140           325           330           335
142 Leu Ser Met Tyr Arg Val Glu Pro Ala Pro Ile Pro Ser Arg Lys Arg
143           340           345           350
145 Ala Phe Ser Val Cys Ala Asp Met Val Gly Ala Gln Arg Glu Ala Gly
146           355           360           365
148 Met Val His Ala Asn Ser Asp Thr Asp Leu Thr Lys Leu Asp Arg Glu
149           370           375           380
151 Lys Thr Phe Glu Thr Ala Glu Ala Tyr His Gln Thr Thr Asp Leu Leu
152 385           390           395           400
154 Ala Lys Val Val Asn Ala Leu Ala Thr Val Lys Pro Pro Pro Ala Glu
155           405           410           415
157 Gln Glu Asp Ala Ala Leu Tyr Gly Gly Tyr His Gly Phe Ser Asp Ser
158           420           425           430
160 Gln Ile Leu Ala Ser Glu Trp Ser Phe Ser Thr Val Asn Glu Phe Thr
161           435           440           445
163 Ser Pro Arg Arg Pro Arg Ala Arg Ala Cys Ser Asp Phe Asn Leu Glu
164           450           455           460
166 Ala Pro Arg Trp Gln Ser Glu Arg Pro Leu Arg Ser Ser His Asn Glu
167 465           470           475           480
169 Trp Thr Trp Ser Gly Asp Asn Gln Gln Ile Gln Glu Ala Phe Asn Gln
170           485           490           495
172 Arg Tyr Lys Gly Gln Gln Arg Ala Asn Gly Ala Ala Asn Ser Thr Met
173           500           505           510
175 Val His Leu Glu Pro Asp Ala Leu Glu Glu Gln Leu Arg Asn Asn His
176           515           520           525
178 Arg Val Pro Val Ala Ser Arg Ser Ser Pro Cys Arg Met Val Cys Asp
179           530           535           540
181 Val Cys Phe Pro Ser Arg Arg Ser Thr Pro Arg Arg Ile Trp Ser Ala
182 545           550           555           560
184 Ser Cys Pro Trp Ser Arg Tyr Pro Arg Val Ser Ser Arg Arg Lys Pro
185           565           570           575
187 Asp Pro Arg Trp Thr Thr Thr Ser Thr Arg Ser Arg Arg Pro Pro Val
188           580           585           590
190 Asn Pro Ile Cys Ala Thr Asp Ala Val Arg His Arg Pro Ser Asn Arg
191           595           600           605
193 Met Ala Ala Trp Pro Ala Ala Ala Ala Gly
194           610           615
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1011
199 <212> TYPE: DNA

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RAW SEQUENCE LISTING

DATE: 06/25/2001

PATENT APPLICATION: US/08/816,011D

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

200 <213> ORGANISM: Caenorhabditis elegans

202 <400> SEQUENCE: 3

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204 aagaatgcag caacggagac atggacattt tcatcgcca tttctttgc cgtaaccgtc 120
205 gtcactacca tcggatcagg taatccagtt ccagtgacaa acattggacg gatattggtg 180
206 atattgttct ccttgcttgg aatacctcta acactggtta ccacgctga cttggcaggt 240
207 aaattcctat ctgaacatct tgtttggtg tatggaaact atttgaaatt aaaatatctc 300
208 atattgtcac gacatcgaaa agaacggaga gagcacgttt gtgagcactg tcacagtcac 360
209 ggaatggggc atgatatgaa tatcgaggag aaaagaattc ctgcattcct ggtattagct 420
210 attctgatag tatatacagc gtttggcggg gtcctaattg caaaattaga gccgtggtct 480
211 ttcttcactt cattctactg gtccttcatt acaatgacta ctgtcgggtt tggcgacttg 540
212 atgcccagaa gggacggata catgtatata atattgctct atatcatttt aggtaaattt 600
213 tcaatgaaaa aaaaaacaaa attcaaaata tttttagggtc ttgcaataac tacaatgtgc 660
214 attgatttgg taggagtaca gtatattcga aagattcatt atttcggaag aaaaattcaa 720
215 gacgctagat ctgcattggc ggttgttaga ggaaaggtag tccttgatc agaactctac 780
216 gcaaatttaa tgcaaaagcg agctcgtaac atgtcccgag aagcttttat agtgagaaat 840
217 ctctatgttt ccaaacacat cataccattc ataccaactg atatccgatg tattcgatat 900
218 attgatcaaa ctgccgatgc tgctaccatt tccacgtcat cgtctgcaat tgatatgcaa 960
219 agttgtagat tttgtcattc aagatattct ctcaatcgtg cattcaaata g 1011

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222 <210> SEQ ID NO: 4

223 <211> LENGTH: 336

224 <212> TYPE: PRT

225 <213> ORGANISM: Drosophila melanogaster

227 <400> SEQUENCE: 4

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229 1 5 10 15
231 Asn Glu Val Lys Lys Asn Ala Ala Thr Glu Thr Trp Thr Phe Ser Ser
232 20 25 30
234 Ser Ile Phe Phe Ala Val Thr Val Val Thr Thr Ile Gly Tyr Gly Asn
235 35 40 45
237 Pro Val Pro Val Thr Asn Ile Gly Arg Ile Trp Cys Ile Leu Phe Ser
238 50 55 60
240 Leu Leu Gly Ile Pro Leu Thr Leu Val Thr Ile Ala Asp Leu Ala Gly
241 65 70 75 80
243 Lys Phe Leu Ser Glu His Leu Val Trp Leu Tyr Gly Asn Tyr Leu Lys
244 85 90 95
246 Leu Lys Tyr Leu Ile Leu Ser Arg His Arg Lys Glu Arg Arg Glu His
247 100 105 110
249 Val Cys Glu His Cys His Ser His Gly Met Gly His Asp Met Asn Ile
250 115 120 125
252 Glu Glu Lys Arg Ile Pro Ala Phe Leu Val Leu Ala Ile Leu Ile Val
253 130 135 140
255 Tyr Thr Ala Phe Gly Gly Val Leu Met Ser Lys Leu Glu Pro Trp Ser
256 145 150 155 160
258 Phe Phe Thr Ser Phe Tyr Trp Ser Phe Ile Thr Met Thr Thr Val Gly
259 165 170 175
261 Phe Gly Asp Leu Met Pro Arg Arg Asp Gly Tyr Met Tyr Ile Ile Leu
262 180 185 190
264 Leu Tyr Ile Ile Leu Gly Lys Phe Ser Met Lys Lys Lys Gln Lys Phe

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001

TIME: 11:28:04

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

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265          195          200          205
267 Lys Ile Phe Leu Gly Leu Ala Ile Thr Thr Met Cys Ile Asp Leu Val
268          210          215          220
270 Gly Val Gln Tyr Ile Arg Lys Ile His Tyr Phe Gly Arg Lys Ile Gln
271 225          230          235          240
273 Asp Ala Arg Ser Ala Leu Ala Val Val Gly Gly Lys Val Val Leu Val
274          245          250          255
276 Ser Glu Leu Tyr Ala Asn Leu Met Gln Lys Arg Ala Arg Asn Met Ser
277          260          265          270
279 Arg Glu Ala Phe Ile Val Glu Asn Leu Tyr Val Ser Lys His Ile Ile
280          275          280          285
282 Pro Phe Ile Pro Thr Asp Ile Arg Cys Ile Arg Tyr Ile Asp Gln Thr
283          290          295          300
285 Ala Asp Ala Ala Thr Ile Ser Thr Ser Ser Ser Ala Ile Asp Met Gln
286 305          310          315          320
288 Ser Cys Arg Phe Cys His Ser Arg Tyr Ser Leu Asn Arg Ala Phe Lys
289          325          330          335
295 <210> SEQ ID NO: 5
296 <211> LENGTH: 51
297 <212> TYPE: DNA
298 <213> ORGANISM: Caenorhabditis elegans
300 <400> SEQUENCE: 5
301 tccattttct ttgccgtaac cgtcgctcact accatcggat acggtaatcc a      51
304 <210> SEQ ID NO: 6
305 <211> LENGTH: 51
306 <212> TYPE: DNA
307 <213> ORGANISM: Caenorhabditis elegans
309 <400> SEQUENCE: 6
310 tcattctact ggtccttcat tacaatgact actgtcgggt ttggcgactt g      51
313 <210> SEQ ID NO: 7
314 <211> LENGTH: 24
315 <212> TYPE: PRT
316 <213> ORGANISM: Drosophila melanogaster
318 <400> SEQUENCE: 7
319 Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly Tyr Gly Phe
320 1          5          10          15
322 Arg Cys Val Thr Asp Glu Cys Pro
323          20
326 <210> SEQ ID NO: 8
327 <211> LENGTH: 24
328 <212> TYPE: PRT
329 <213> ORGANISM: Drosophila melanogaster
331 <400> SEQUENCE: 8
332 Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly Tyr Gly Phe
333 1          5          10          15
335 Arg Cys Val Thr Glu Gln Cys Ala
336          20
339 <210> SEQ ID NO: 9
340 <211> LENGTH: 24

```

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<210> 65

<211> 4

<212> PRT

<213> Artificial Sequence

see item 11 on Error Summary Sheet

<400> 65

Thr Trp Thr Phe

1

FSI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/08/816,011D

DATE: 06/25/2001

TIME: 11:28:05

Input Set : A:\11420121.app

Output Set: N:\CRF3\06252001\H816011D.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:840 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
 L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
 L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1069 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
 L:1125 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51
 L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
 L:1189 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
 L:1195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:53
 L:1226 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
 L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
 L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:56
 L:1409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
 L:1430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
 L:1463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60
 L:1493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61
 L:1690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64
 L:1699 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:1699 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:

Attachment for PTO-948 (Rev. 03/01, or earlier)

6/18/01

The below text replaces the pre-printed text under the heading, "Information on How to Effect Drawing Changes," on the back of the PTO-948 (Rev. 03/01, or earlier) form.

INFORMATION ON HOW TO EFFECT DRAWING CHANGES

1. Correction of Informalities -- 37 CFR 1.85

New corrected drawings must be filed with the changes incorporated therein. Identifying indicia, if provided, should include the title of the invention, inventor's name, and application number, or docket number (if any) if an application number has not been assigned to the application. If this information is provided, it must be placed on the front of each sheet and centered within the top margin. If corrected drawings are required in a Notice of Allowability (PTOL-37), the new drawings **MUST** be filed within the **THREE MONTH** shortened statutory period set for reply in the Notice of Allowability. Extensions of time may **NOT** be obtained under the provisions of 37 CFR 1.136(a) or (b) for filing the corrected drawings after the mailing of a Notice of Allowability. The drawings should be filed as a separate paper with a transmittal letter addressed to the Official Draftsperson.

2. Corrections other than Informalities Noted by Draftsperson on form PTO-948.

All changes to the drawings, other than informalities noted by the Draftsperson, **MUST** be made in the same manner as above except that, normally, a highlighted (preferably red ink) sketch of the changes to be incorporated into the new drawings **MUST** be approved by the examiner before the application will be allowed. No changes will be permitted to be made, other than correction of informalities, unless the examiner has approved the proposed changes.

Timing of Corrections

Applicant is required to submit the drawing corrections within the time period set in the attached Office communication. See 37 CFR 1.85(a).

Failure to take corrective action within the set period will result in **ABANDONMENT** of the application.